GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2005, 06:54:38 ; Search time 1052 Seconds
(without alignments)
9902.920 Million cell updates/sec

Title: US-09-936-506-1
Perfect score: 215
Sequence: 1 ataacggctagcctgaggag.....gacagagagcagggaaccgc 215

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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6: gb_pat:*
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13: gb_un:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	215	100.0	215	6	BD273753	BD273753 Expressio
2	215	100.0	215	6	BD273754	BD273754 Expressio
3	215	100.0	215	6	AX036038	AX036038 Sequence
4	215	100.0	215	6	AX036039	AX036039 Sequence
5	215	100.0	533	6	AR084816	AR084816 Sequence
6	215	100.0	533	6	I21401	I21401 Sequence 2
7	215	100.0	533	6	I95741	I95741 Sequence 2
8	215	100.0	2465	6	E12384	E12384 Human cDNA
9	215	100.0	2691	6	CQ812310	CQ812310 Sequence
10	215	100.0	2691	6	CQ818823	CQ818823 Sequence
11	215	100.0	2691	6	AR262810	AR262810 Sequence
12	215	100.0	2691	9	HUMHSP70D	M11717 Human heat
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14	214.6	99.8	488	9	S52686	S52686 HLA class I
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19	214	99.5	179894	9	AL662834	AL662834 Human DNA
c 20	214	99.5	180283	9	AF134726	AF134726 Homo sapi
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23	212.4	98.8	2700	9	HUMMHHSP	M59828 Human MHC c
24	212.4	98.8	97255	2	CR759915	CR759915 Homo sapi
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31	203	94.4	214	6	AX036046	AX036046 Sequence
32	191.4	89.0	2412	6	AR531603	AR531603 Sequence
33	187.4	87.2	420	6	AR413190	AR413190 Sequence
34	187.4	87.2	420	6	AX970024	AX970024 Sequence
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c 36	186.2	86.6	511	6	AX194930	AX194930 Sequence
37	173.4	80.7	2379	9	BC002453	BC002453 Homo sapi
38	163.6	76.1	2876	6	AX770499	AX770499 Sequence
39	163.6	76.1	2876	9	HUMMHHSP2	M59830 Human MHC c
c 40	163.6	76.1	3533	9	AY559742	AY559742 Homo sapi
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44	156.8	72.9	2458	6	AR531604	AR531604 Sequence
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ALIGNMENTS

RESULT 1
BD273753
LOCUS BD273753 215 bp DNA linear PAT 17-JUL-2003
DEFINITION Expression.
ACCESSION BD273753
VERSION BD273753.1 GI:33083521
KEYWORDS JP 2002537843-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 215)
AUTHORS Coste,H.J. and Ellis,J.H.
TITLE Expression
JOURNAL Patent: JP 2002537843-A 1 12-NOV-2002;
GLAXO GROUP LTD
COMMENT OS Homo sapiens (human)
PN JP 2002537843-A/1
PD 12-NOV-2002
PF 09-MAR-2000 JP 2000603406
PR 11-MAR-1999 GB 9905498.3
PI HERVE JEAN-CLEMENT COSTE,JONATHAN HENRY ELLIS PC C12N15/09,A61K38/44,A61K39/00,A61K48/00,C07K14/46,C12N5/10, PC C12P21/02,
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CC Expression
FH Key Location/Qualifiers
FT source 1. .215
FT /organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
source 1. .215
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/mol_type="genomic DNA"
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ORIGIN

Query Match 100.0%; Score 215; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.3e-46;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
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Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
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LOCUS       BD273754                 215 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Expression.
ACCESSION   BD273754
VERSION     BD273754.1  GI:33083522
KEYWORDS    JP 2002537843-A/2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 215)
  AUTHORS   Coste,H.J. and Ellis,J.H.
  TITLE     Expression
  JOURNAL   Patent: JP 2002537843-A 2 12-NOV-2002;
            GLAXO GROUP LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002537843-A/2
            PD   12-NOV-2002
            PF   09-MAR-2000 JP 2000603406
            PR   11-MAR-1999 GB    9905498.3
            PI   HERVE JEAN-CLEMENT COSTE,JONATHAN HENRY ELLIS PC
            C12N15/09,A61K38/44,A61K39/00,A61K48/00,C07K14/46,C12N5/10, PC
            C12P21/02,
            PC   C12N15/00,C12N5/00,A61K37/50
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.3e-46;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
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Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
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Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
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Db        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215


RESULT 3
AX036038
LOCUS       AX036038                 215 bp    DNA     linear   PAT 15-NOV-2000
DEFINITION  Sequence 1 from Patent WO0053785.
ACCESSION   AX036038
VERSION     AX036038.1  GI:11191577
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Coste,H.J. and Ellis,J.H.
  TITLE     Expression
  JOURNAL   Patent: WO 0053785-A 1 14-SEP-2000;
            COSTE HERVE JEAN CLEMENT (FR) ; GLAXO GROUP LTD (GB) ; ELLIS
            JONATHAN HENRY (GB)
FEATURES              Location/Qualifiers
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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
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Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
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RESULT 4
AX036039
LOCUS       AX036039                 215 bp    RNA     linear   PAT 15-NOV-2000
DEFINITION  Sequence 2 from Patent WO0053785.
ACCESSION   AX036039
VERSION     AX036039.1  GI:11191578
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Coste,H.J. and Ellis,J.H.
  TITLE     Expression
  JOURNAL   Patent: WO 0053785-A 2 14-SEP-2000;
            COSTE HERVE JEAN CLEMENT (FR) ; GLAXO GROUP LTD (GB) ; ELLIS
            JONATHAN HENRY (GB)
FEATURES              Location/Qualifiers
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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
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Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
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Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
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Db        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215


RESULT 5
AR084816
LOCUS       AR084816                533 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 2 from patent US 5981224.
ACCESSION   AR084816
VERSION     AR084816.1  GI:10011587
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 533)
  AUTHORS   Kowalski,J., Gilbert,S. and Zamb,T.J.
  TITLE     Bovine heat shock promoter and uses thereof
  JOURNAL   Patent: US 5981224-A 2 09-NOV-1999;
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Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
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Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
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RESULT 6
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LOCUS       I21401                  533 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 2 from patent US 5521084.
ACCESSION   I21401
VERSION     I21401.1  GI:1601755
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 533)
  AUTHORS   Kowalski,J., Gilbert,S. and Zamb,T.J.
  TITLE     Bovine heat shock promoter and uses thereof
  JOURNAL   Patent: US 5521084-A 2 28-MAY-1996;
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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
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RESULT 7
I95741
LOCUS       I95741                  533 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 2 from patent US 5733745.
ACCESSION   I95741
VERSION     I95741.1  GI:3940211
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 533)
  AUTHORS   Kowalski,J., Gilbert,S. and Zamb,T.J.
  TITLE     Bovine heat shock promoter and uses thereof
  JOURNAL   Patent: US 5733745-A 2 31-MAR-1998;
FEATURES             Location/Qualifiers
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Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
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Db        415 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 449


RESULT 8
E12384
LOCUS       E12384                  2465 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Human cDNA encoding HSP70.
ACCESSION   E12384
VERSION     E12384.1  GI:3251217
KEYWORDS    JP 1996322577-A/1.
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 2465)
  AUTHORS   Demura,H., Nomura,K., Shimizu,S., Raari,T.H. and Hisakawa,Y.
  TITLE     TRANSCRIPTIONAL ABNORMALITY OF INTRACELLULAR HSP70MRNA UNDER
            SUSTAINED STRESS LOAD CONTAINING HUMAN ACUTENESS AND CHRONICITY AND
            ITS APPLICATION (APPLICATION OF BOTH TRANSCRIPTIONAL EXPRESSION OF
            NEW HUMAN INTRACELLULAR SHSP70MRNA AND TRANSCRIPTIONAL ABNORMALITY
            OF HSP70 MRNA)
  JOURNAL   Patent: JP 1996322577-A 1 10-DEC-1996;
            HOKEN KAGAKU KENKYUSHO:KK
COMMENT     OS   Homo sapiens (human)
            PN   JP 1996322577-A/1
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            PF   01-JUN-1995 JP 1995158581
            PI   DEMURA HIROSHI, NOMURA KAORU, SHIMIZU SHOICHI, PI   RAARI
            TABURIYU HANKINZU,
            PI   HISAKAWA YOSHIZO
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Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
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Db        168 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 227

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              |||||||||||||||||||||||||||||||||||
Db        228 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 262


RESULT 9
CQ812310
LOCUS       CQ812310               2691 bp    DNA     linear   PAT 24-MAY-2004
DEFINITION  Sequence 62 from Patent WO2004038020.
ACCESSION   CQ812310
VERSION     CQ812310.1  GI:47601930
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wittig,R., Poustka,A., Mollenhauer,J. and Schadendorf,D.
  TITLE     Target genes for the diagnosis and treatment of cancer
  JOURNAL   Patent: WO 2004038020-A 62 06-MAY-2004;
            Deutsches Krebsforschungszentrum Stiftung des oeffentliche n Rechts
            (DE)
FEATURES              Location/Qualifiers
     source           1. .2691
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
     misc_feature     1. .2691
                      /note="M11717"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.1e-46;
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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGCGTCGAGTTT 393

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 453

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              |||||||||||||||||||||||||||||||||||
Db        454 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 488


RESULT 10
CQ818823
LOCUS       CQ818823               2691 bp    DNA     linear   PAT 07-JUN-2004
DEFINITION  Sequence 6 from Patent WO2004039412.
ACCESSION   CQ818823
VERSION     CQ818823.1  GI:48427426
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Doiron,B., Pownall,S., Cheung,A. and Hsu,E.
  TITLE     Compositions for cancer treatment
  JOURNAL   Patent: WO 2004039412-A 6 13-MAY-2004;
            Engene, Inc. (CA)
FEATURES              Location/Qualifiers
     source           1. .2691
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGCGTCGAGTTT 120
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Db        334 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGCGTCGAGTTT 393

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 453
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Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              |||||||||||||||||||||||||||||||||||
Db        454 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 488


RESULT 11
AR262810
LOCUS       AR262810                2691 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 1 from patent US 6331388.
ACCESSION   AR262810
VERSION     AR262810.1  GI:28074512
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2691)
  AUTHORS   Malkovsky,M. and Wells,A.D.
  TITLE     Immune response enhancer
  JOURNAL   Patent: US 6331388-A 1 18-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .2691
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.1e-46;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 393

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
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Db        394 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 453

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              |||||||||||||||||||||||||||||||||||
Db        454 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 488


RESULT 12
HUMHSP70D
LOCUS       HUMHSP70D               2691 bp    DNA     linear   PRI 08-NOV-1994
DEFINITION  Human heat shock protein (hsp 70) gene, complete cds.
ACCESSION   M11717 M15432
VERSION     M11717.1  GI:184416
KEYWORDS    HSP70 gene; heat shock protein.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2691)
  AUTHORS   Hunt,C. and Morimoto,R.I.
  TITLE     Conserved features of eukaryotic hsp70 genes revealed by comparison
            with the nucleotide sequence of human hsp70
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 82 (19), 6455-6459 (1985)
  MEDLINE   86016721
   PUBMED   3931075
REFERENCE   2  (bases 94 to 293)
  AUTHORS   Morgan,W.D., Williams,G.T., Morimoto,R.I., Greene,J., Kingston,R.E.
            and Tjian,R.
  TITLE     Two transcriptional activators, CCAAT-box-binding transcription
            factor and heat shock transcription factor, interact with a human
            hsp70 gene promoter
  JOURNAL   Mol. Cell. Biol. 7 (3), 1129-1138 (1987)
  MEDLINE   87172780
   PUBMED   3561411
COMMENT     Original source text: Homo sapiens DNA.
            [2]  revises [1]. Sequence revised July 30, 1992.
FEATURES             Location/Qualifiers
     source          1. .2691
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="6p21.3"
     mRNA            274. .2691
                     /product="70 kDa hsp mRNA"
     gene            489. .2411
                     /gene="HSPA1L"
     CDS             489. .2411
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                     /note="70 kDa"
                     /codon_start=1
                     /product="heat shock protein"
                     /protein_id="AAA52697.1"
                     /db_xref="GI:386785"
                     /db_xref="GDB:G00-120-058"
                     /translation="MAKAAAVGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAF
                     TDTERLIGDAAKNQVALNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPK
                     VQVSYKGETKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKD
                     AGVIAGLNVLRIINEPTAAAIAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFE
                     VKATAGDTHLGGEDFDNRLVNHFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSS
                     STQASLEIDSLFEGIDFYTSITRARFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDL
                     VLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVGYGAAVQAAILMGDKSENVQDLL
                     LLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGERAMT
                     KDNNLLGRFELSGIPPAPGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDKGR
                     LSKEEIERMVQEAEKYKAEDEVQRERVSAKNALESYAFNMKSAVEDEGLKGKISEADK
                     KKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQVCNPIISGLYQGAGGPGPGGFGAQ
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ORIGIN

  Query Match             100.0%;  Score 215;  DB 9;  Length 2691;
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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
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Db        274 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
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Db        334 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 393

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 453

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
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Db        454 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 488


RESULT 13
AB018045
LOCUS       AB018045                4360 bp    DNA     linear   PRI 14-APR-2000
DEFINITION  Homo sapiens HSP70-1 gene for heat shock protein 72, spliced
            variant, partial cds.
ACCESSION   AB018045
VERSION     AB018045.1  GI:4691417
KEYWORDS    HSP70-1; heat shock protein 72; HSP70-Hom; alternative splicing.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Shimizu,S., Nomura,K., Ujihara,M. and Demura,H.
  TITLE     An additional exon of stress-inducible heat shock protein 70 gene
            (HSP70-1)
  JOURNAL   Biochem. Biophys. Res. Commun. 257 (1), 193-198 (1999)
  MEDLINE   99194576
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   PUBMED   10092532
REFERENCE   2  (bases 1 to 4360)
  AUTHORS   Nomura,K. and Shimizu,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-SEP-1998) Kaoru Nomura, Tokyo Women's Medical
            University, Department of Medicine 2; 8-1 Kawadacho, Shinjyuku-ku,
            Tokyo 162-8666, Japan (E-mail:nomura7@parkcity.ne.jp,
            Tel:81-3-3353-8111(ex.39223), Fax:81-3-3357-6475)
COMMENT     Sequence updated (26-Oct-1998).
FEATURES             Location/Qualifiers
     source          1. .4360
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                     /db_xref="taxon:9606"
                     /chromosome="6"
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     gene            complement(1. .196)
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     misc_feature    complement(1. .196)
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     gene            2323. .4360
                     /gene="HSP70-1"
     exon            2323. .2679
                     /gene="HSP70-1"
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                     /note="spliced variant"
                     /codon_start=1
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                     /db_xref="GI:4691418"
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     exon            3443. .3954
                     /gene="HSP70-1"
                     /note="alternative splicing
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     exon            3955. .>4360
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Db       3434 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 3493

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
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Db       3494 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 3553

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
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Db       3554 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 3613

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
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Db       3614 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 3648


RESULT 14
S52686
LOCUS       S52686                   488 bp    DNA     linear   PRI 08-MAY-1993
DEFINITION  HLA class III polymorphic region: HSP70-1=heat shock protein 70 (5'
            region) [human, PGF, WT49, WT51, Genomic, 488 nt].
ACCESSION   S52686
VERSION     S52686.1  GI:263578
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   Cascino,I., Sorrentino,R. and Tosi,R.
  TITLE     Strong genetic association between HLA-DR3 and a polymorphic
            variation in the regulatory region of the HSP70-1 gene
  JOURNAL   Immunogenetics 37 (3), 177-182 (1993)
  MEDLINE   93131289
   PUBMED   8420825
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 122511] from the original journal article.
COMMENT     Region: HLA class III polymorphic region.
FEATURES             Location/Qualifiers
     source          1. .488
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
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     gene            1. .488
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                     /note="heat shock protein 70"
ORIGIN

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  Best Local Similarity   99.5%;  Pred. No. 1.6e-46;
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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
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Db        274 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        334 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTY 393

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
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Db        394 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 453

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              |||||||||||||||||||||||||||||||||||
Db        454 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 488


RESULT 15
CQ806661
LOCUS       CQ806661                 5387 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 111 from Patent WO2004035803.
ACCESSION   CQ806661
VERSION     CQ806661.1  GI:47112043
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
            Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
            Marx,A.
  TITLE     Method and nucleic acids for the improved treatment of breast cell
            proliferative disorders
  JOURNAL   Patent: WO 2004035803-A 111 29-APR-2004;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .5387
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Query Match 99.5%; Score 214; DB 6; Length 5387;
Best Local Similarity 100.0%; Pred. No. 2e-46;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1982 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 2041

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2042 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 2101

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2102 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 2161

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
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Db       2162 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 2195
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Title: US-09-936-506-1
Perfect score: 215
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	215	100.0	215	3	AAA94756	Aaa94756 Human HSP
	3	215	100.0	2691	6	ABA99140	Aba99140 Human hsp
	4	215	100.0	2691	6	ABK83917	Abk83917 Human cDN
	5	215	100.0	2691	10	ADD14739	Add14739 Human src
	6	214	99.5	2732	10	ADD29869	Add29869 Human tum
	7	214	99.5	2767	12	ADQ87261	Adq87261 Human tum
	8	214	99.5	2767	12	ADQ84979	Adq84979 Human tum
	9	214	99.5	2767	13	ADQ83802	Adq83802 Human tum
	10	214	99.5	5387	13	ADS89095	Ads89095 Human HSP
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	19	195	90.7	2387	13	ACN38447	Acn38447 Tumour-as
	20	191.4	89.0	2412	12	ADE76979	Ade76979 Human cDN
	21	186.8	86.9	2302	3	AAA15622	Aaa15622 Human hea
c	22	186.2	86.6	511	4	AAH88560	Aah88560 CNS disor
	23	185.2	86.1	2302	3	AAA15621	Aaa15621 Human hea
c	24	163.6	76.1	506	12	ACH73362	Ach73362 Human gen
	25	163.6	76.1	2876	8	ACA89884	Aca89884 Gene diff
	26	156.8	72.9	2458	12	ADE76980	Ade76980 Human cDN
	27	156.8	72.9	2513	10	ADD29868	Add29868 Human tum
	28	145.2	67.5	595	6	ABQ30839	Abq30839 Oligonucl
c	29	145.2	67.5	595	6	ABQ30838	Abq30838 Oligonucl
	30	145.2	67.5	596	6	ABQ34141	Abq34141 Oligonucl
c	31	145.2	67.5	596	6	ABQ34140	Abq34140 Oligonucl
c	32	145.2	67.5	5387	13	ADS89452	Ads89452 Oligonucl
c	33	145.2	67.5	9899	6	ABL34442	Abl34442 Human imm
c	34	134	62.3	595	6	ABQ30841	Abq30841 Oligonucl
	35	134	62.3	595	6	ABQ30840	Abq30840 Oligonucl
c	36	134	62.3	596	6	ABQ34139	Abq34139 Oligonucl
	37	134	62.3	596	6	ABQ34138	Abq34138 Oligonucl
	38	134	62.3	5387	13	ADS89451	Ads89451 Oligonucl
	39	134	62.3	9899	6	ABL34443	Abl34443 Human imm
	40	116.6	54.2	2460	10	ADF76348	Adf76348 Novel hum
	41	116.6	54.2	2460	12	ADQ87260	Adq87260 Human tum
	42	116.6	54.2	2460	12	ADQ83801	Adq83801 Human tum
	43	116.6	54.2	2460	13	ADQ84978	Adq84978 Human tum
	44	116.6	54.2	2460	13	ACN38446	Acn38446 Tumour-as
c	45	113.8	52.9	5387	13	ADS89726	Ads89726 Oligonucl

ALIGNMENTS

RESULT 1
AAA94740
ID AAA94740 standard; DNA; 215 BP.
XX
AC AAA94740;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human HSP70A 5' untranslated region DNA sequence.
XX
KW Human; HSP70A; 5' UTR; untranslated region; heat shock protein;
KW translation efficiency; vaccine; bacterial; viral; parasitic infection;
KW immune-related disease; contraceptive; gene therapy; cancer;
KW cardiovascular disorder; cystic fibrosis; ds.
XX
OS Homo sapiens.
XX
PN WO200053785-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-EP002031.
XX
PR 11-MAR-1999; 99GB-00005498.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Coste HJ, Ellis JH;
XX
DR WPI; 2000-594331/56.
XX
PT Human heat shock protein 5' untranslated region (UTR) transcribed to
PT provide an RNA molecule having UTR that increases translation efficiency
PT of polypeptides, useful for treating deficiency in expression of the
PT polypeptide.
XX
PS Claim 7; Page 28; 44pp; English.
XX
CC The present sequence is the 5' untranslated region (UTR) of human heat
CC shock protein (Hsp) 70A gene. This sequence has a high potential to form
CC secondary structures. This sequence can be used to increase the
CC translation efficiency of a polypeptide. The present sequence may be
CC useful in therapeutic or prophylactic vaccination for preventing

CC bacterial, viral and parasitic infections and also for treating immune-
CC related diseases and for contraceptive purposes. In addition, the present
CC sequence may be useful in gene therapy of various disorders such as
CC cancer, cardiovascular disorders and cystic fibrosis
XX
SQ Sequence 215 BP; 41 A; 71 C; 63 G; 40 T; 0 U; 0 Other;

Query Match 100.0%; Score 215; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.6e-55;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              |||||||||||||||||||||||||||||||||||
Db        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
```

RESULT 2
AAA94756
ID AAA94756 standard; mRNA; 215 BP.
XX
AC AAA94756;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human HSP70A 5' untranslated region mRNA sequence.
XX
KW Human; HSP70A; 5' UTR; untranslated region; heat shock protein;
KW translation efficiency; vaccine; bacterial; viral; parasitic infection;
KW immune-related disease; contraceptive; gene therapy; cancer;
KW cardiovascular disorder; cystic fibrosis; ss.
XX
OS Homo sapiens.
XX
PN WO200053785-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-EP002031.
XX
PR 11-MAR-1999; 99GB-00005498.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Coste HJ, Ellis JH;
XX
DR WPI; 2000-594331/56.
XX
PT Human heat shock protein 5' untranslated region (UTR) transcribed to
PT provide an RNA molecule having UTR that increases translation efficiency
PT of polypeptides, useful for treating deficiency in expression of the
PT polypeptide.
XX
PS Disclosure; Page 3; 44pp; English.
XX
CC The present sequence is the 5' untranslated region (UTR) mRNA of human
CC heat shock protein (Hsp) 70A gene. This sequence has a high potential to
CC form secondary structures. This sequence can be used to increase the
CC translation efficiency of a polypeptide. The present sequence may be
CC useful in therapeutic or prophylactic vaccination for preventing
CC bacterial, viral and parasitic infections and also for treating immune-
CC related diseases and for contraceptive purposes. In addition, the present
CC sequence may be useful in gene therapy of various disorders such as
CC cancer, cardiovascular disorders and cystic fibrosis
XX
SQ Sequence 215 BP; 41 A; 71 C; 63 G; 0 T; 40 U; 0 Other;

Query Match 100.0%; Score 215; DB 3; Length 215;
Best Local Similarity 81.4%; Pred. No. 6.6e-55;
Matches 175; Conservative 40; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              |:||||||:||||:|||||||:||:|||||||:||||:|||:::::|||||:|||:|||
Db          1 AUAACGGCUAGCCUGAGGAGCUGCUGCGACAGUCCACUACCUUUUUCGAGAGUGACUCCC 60

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              |::|:||||||||::|||||||||||||:|:|||||:||||||||||||||||:||||:::
Db         61 GUUGUCCCAAGGCUUCCCAGAGCGAACCUGUGCGGCUGCAGGCACCGGCGCGUCGAGUUU 120

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||:|||||||||||||||:|::|:||||||:||||:|::|||:::|||||||||||
Db        121 CCGGCGUCCGGAAGGACCGAGCUCUUCUCGCGGAUCCAGUGUUCCGUUUCCAGCCCCCAA 180

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              :|:||||||||||||||||||||||||||||||||
Db        181 UCUCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
```

RESULT 3
ABA99140
ID ABA99140 standard; cDNA; 2691 BP.
XX
AC ABA99140;
XX
DT 23-MAY-2002 (first entry)
XX
DE Human hsp72 encoding sequence.
XX
KW Human; hsp72; heat shock protein; cytostatic; antibacterial;
KW antiparasitic; MHC class I; ss.
XX
OS Homo sapiens.
XX
PN US6331388-B1.
XX
PD 18-DEC-2001.
XX
PF 17-OCT-1997; 97US-00955565.
XX
PR 17-OCT-1997; 97US-00955565.
XX
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Malkovsky M, Wells AD;
XX
DR WPI; 2002-138381/18.
XX
PT Increasing expression of an MHC class I molecule in a cell, useful in
PT increasing antigen presentation and enhancing immune recognition of cells
PT infected with pathogens, by expressing a heat shock protein introduced by
PT a vector.
XX
PS Example 1; Fig 1; 89pp; English.
XX
CC This invention relates to increasing expression of an MHC class I
CC molecule in a target cell, infected with a pathogen that is processed by
CC the MHC class I endogenous pathway. The method of expressing a HSP is
CC achieved by the introduction of an expression vector encoding HSP to
CC produce a transfected cell with increased expression of at least one MHC
CC class I molecule. The method is cytostatic, antibacterial and
CC antiparasitic. The method can be used to increase expression of an MHC
CC class I molecule in a target cell and to increase presentation of an
CC antigen on a cell surface by an MHC class I molecule. The method can
CC enhance the immunogenicity of the endogenous antigen in vivo, by
CC enhancing the generation of antibodies to an otherwise poorly immunogenic

CC antigen or cell. The method can be used in the immunotherapy of cancer
CC and pathogen infections, and for enhancing or reducing radiation
CC resistance of cells. The expression of the heat shock protein in a cell
CC enhances the presentation of endogenous antigens by MHC class I molecules
CC onto the cell surface in vitro, and can enhance the immunogenicity of the
CC endogenous antigen in vivo, by enhancing the generation of antibodies to
CC an otherwise poorly immunogenic antigen or cell. This sequence represents
CC the cDNA of human hsp72
XX
SQ Sequence 2691 BP; 600 A; 780 C; 831 G; 480 T; 0 U; 0 Other;

Query Match 100.0%; Score 215; DB 6; Length 2691;
Best Local Similarity 100.0%; Pred. No. 1.1e-54;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 393

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 453

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              |||||||||||||||||||||||||||||||||||
Db        454 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 488
```

RESULT 4
ABK83917
ID ABK83917 standard; cDNA; 2691 BP.
XX
AC ABK83917;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #488.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN WO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US030821.
XX
PR 03-OCT-2000; 2000US-0237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression of
PT genes associated with granulocyte activation, which serves as diagnostic
PT markers that is useful for monitoring disease states and drug toxicity.
XX
PS Claim 1; SEQ ID NO 488; 114pp; English.
XX

CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2691 BP; 600 A; 780 C; 831 G; 480 T; 0 U; 0 Other;

Query Match 100.0%; Score 215; DB 6; Length 2691;
Best Local Similarity 100.0%; Pred. No. 1.1e-54;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 393

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 453

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              |||||||||||||||||||||||||||||||||||
Db        454 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 488
```

RESULT 5
ADD14739
ID ADD14739 standard; cDNA; 2691 BP.
XX
AC ADD14739;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human src biomarker polynucleotide SEQ ID NO:133.
XX
KW predictor set; protein tyrosine kinase activity modulator;
KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
KW gene therapy; drug sensitivity; genetic profile; cancer; human; gene; ss.
XX

```
OS   Homo sapiens.
XX
PN   WO2003062395-A2.
XX
PD   31-JUL-2003.
XX
PF   17-JAN-2003; 2003WO-US001981.
XX
PR   18-JAN-2002; 2002US-0350061P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Huang F,  Fairchild CR,  Lee FY,  Shaw P;
XX
DR   WPI; 2003-636735/60.
DR   P-PSDB; ADD14137.
XX
PT   New polynucleotides and polypeptides for predicting the activity of
PT   compounds that interact with protein tyrosine kinases and/or protein
PT   tyrosine kinase pathways.
XX
PS   Claim 2; SEQ ID NO 133; 139pp; English.
XX
CC   The present invention describes a predictor set comprising a plurality of
CC   polynucleotides or polypeptides whose expression pattern is predictive of
CC   the response of cells to treatment with a compound that modulates protein
CC   tyrosine kinase activity or members of the protein tyrosine kinase
CC   pathway. Also described: (1) predicting whether a compound is capable of
CC   modulating the activity of cells, comprising obtaining a sample of cells,
CC   determining whether the cells express a plurality of markers, and
CC   correlating the expression of the markers to the compound's ability to
CC   modulate the activity of the cells; (2) a plurality of cell lines for
CC   identifying polynucleotides and polypeptides whose expression levels
CC   correlate with compound sensitivity or resistance of cells associated
CC   with a disease state; and (3) identifying polynucleotides and
CC   polypeptides that predict compound sensitivity or resistance of cells
CC   associated with a disease state, comprising subjecting the plurality of
CC   cell lines to one or more compounds, analysing the expression pattern of
CC   a microarray of polynucleotides or polypeptides, and selecting
CC   polynucleotides or polypeptides that predict the sensitivity or
CC   resistance of cells associated with a disease state by using the
CC   expression pattern of the microarray. The polynucleotides and
CC   polypeptides have cytostatic activities, and can be used in gene therapy.
CC   The polynucleotides and polypeptides are useful in predicting the
CC   activity of compounds that interact with protein tyrosine kinases and/or
CC   protein tyrosine kinase pathways. These may be used in determining drug
CC   sensitivity in patients to allow the development of individualized
CC   genetic profiles which aid in treating diseases and disorders (e.g.
CC   cancer) based on patient response at a molecular level. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 2691 BP; 600 A; 780 C; 831 G; 480 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 215;  DB 10;  Length 2691;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-54;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 393

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 453

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              |||||||||||||||||||||||||||||||||||
Db        454 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 488
```

```
RESULT 6
ADD29869
ID   ADD29869 standard; mRNA; 2732 BP.
XX
AC   ADD29869;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human tumour suppressor mRNA SEQ ID NO:300.
XX
KW   ss; human; tumour suppressor; cancer; cancer; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003058201-A2.
XX
PD   17-JUL-2003.
XX
PF   31-DEC-2002; 2002WO-US041825.
XX
PR   31-DEC-2001; 2001US-0345317P.
XX
PA   (QUAR-) QUARK BIOTECH INC.
PA   (CLEV-) CLEVELAND CLINIC FOUND.
XX
PI   Feinstein E,  Gudkov AV;
XX
DR   WPI; 2003-598393/56.
XX
PT   Diagnosing cancer comprises determining the polypeptide or polynucleotide
PT   levels e.g., hepatic lipase, in a sample from a subject, where a higher
PT   level compared to that in a subject free of cancer is indicative of
PT   cancer.
XX
PS   Disclosure; SEQ ID NO 300; 272pp; English.
XX
CC   The invention relates to a novel method for diagnosing a cancer in a
CC   subject. the method comprises determining, in a sample from the subject,
CC   the level of at least one polypeptide, where a higher level of the
CC   polypeptide compared to the level of the polypeptide in a subject free of
CC   cancer is indicative of cancer. The polypeptide is selected from any of
CC   the polypeptides encoded by the polynucleotides listed in the
CC   specification and polypeptides which are at least 70% homologous to the
CC   polypeptides. The method of the invention has cytostatic activity, and
CC   may have a use in gene therapy. The method is useful in identifying
CC   markers specific for one or several types of cancer, depending on the
CC   tissue origin, which may be used in numerous diagnostic and prognostic
CC   applications as well as cancer type-specific targets for therapeutic
CC   intervention. The compounds that modulate the activity of a tumour
CC   suppressor gene are useful in the treatment of cancer or as anti-cancer
CC   drugs. The present sequence represents a polynucleotide of the invention.
XX
SQ   Sequence 2732 BP; 608 A; 787 C; 840 G; 497 T; 0 U; 0 Other;

  Query Match           99.5%;  Score 214;  DB 10;  Length 2732;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-54;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 393

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 453

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||||||||||||||||||||||||||||
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```
Db        454 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 487

RESULT 7
ADQ87261
ID   ADQ87261 standard; cDNA; 2767 BP.
XX
AC   ADQ87261;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human tumour-associated antigenic target (TAT) cDNA sequence #4138.
XX
KW   human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW   cancer; cell proliferative disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004060270-A2.
XX
PD   22-JUL-2004.
XX
PF   15-OCT-2003; 2003WO-US029126.
XX
PR   18-OCT-2002; 2002US-0418988P.
XX
PA   (GETH ) GENENTECH INC.
PA   (WUTD/) WU T D.
PA   (ZHOU/) ZHOU Y.
XX
PI   Wu TD,  Zhou Y;
XX
DR   WPI; 2004-534300/51.
XX
PT   New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT   preventing or treating cell proliferative disorders such as cancer.
XX
PS   Claim 1; SEQ ID NO 4138; 5504pp; English.
XX
CC   The present invention describes an isolated tumour-associated antigenic
CC   target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC   sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC   (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC   sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC   (c). Also described: (1) an expression vector comprising the above
CC   nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC   a process for producing a polypeptide; (4) an isolated polypeptide
CC   comprising: (a) an amino acid sequence encoded by any of the above
CC   nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC   length coding region of the above nucleotide sequences; or (c) a sequence
CC   having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC   comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC   an isolated antibody that binds to the above polypeptide; (7) a process
CC   for producing the antibody; (8) an isolated oligopeptide that binds to
CC   the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC   binding organic molecule that binds to the above polypeptide; (10) a
CC   composition of matter comprising the above (chimeric) polypeptide,
CC   antibody, oligopeptide or TAT binding organic molecule, in combination
CC   with a carrier; (11) an article of manufacture comprising a container and
CC   the composition of matter contained within the container; (12) methods of
CC   inhibiting the growth of a cell that expresses the above protein, where
CC   the growth of the cell is at least in part dependent upon a growth
CC   potentiating effect of the above protein; (13) a method of
CC   therapeutically treating a mammal having a cancerous tumour comprising
CC   cells that express the above protein; (14) a method of determining the
CC   presence of a protein in a sample suspected of containing the protein
CC   described above; (15) methods of diagnosing the presence of a tumour in a
CC   mammal; (16) a method for treating or preventing a cell proliferative
CC   disorder associated with increased expression or activity of the above
CC   protein; and (17) a method of binding an antibody, oligopeptide or
CC   organic molecule to a cell that expresses the protein described above.
CC   The TAT sequences have cytostatic activities, and can be used in gene
CC   therapy. The composition and methods are useful for diagnosing,
CC   preventing or treating cancer. The composition is also used for preparing
CC   a medicament for the therapeutic treatment or diagnostic detection of a
CC   cell proliferative disorder or cancer. The present sequence represents a
CC   human TAT cDNA sequence from the present invention.
XX
SQ   Sequence 2767 BP; 621 A; 808 C; 854 G; 484 T; 0 U; 0 Other;

  Query Match             99.5%;  Score 214;  DB 12;  Length 2767;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-54;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 421

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 481

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 541

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||||||||||||||||||||||||||||
Db        542 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 575


RESULT 8
ADQ84979
ID   ADQ84979 standard; cDNA; 2767 BP.
XX
AC   ADQ84979;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human tumour-associated antigenic target (TAT) cDNA sequence #1793.
XX
KW   human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW   cancer; cell proliferative disorder; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004060270-A2.
XX
PD   22-JUL-2004.
XX
PF   15-OCT-2003; 2003WO-US029126.
XX
PR   18-OCT-2002; 2002US-0418988P.
XX
PA   (GETH ) GENENTECH INC.
PA   (WUTD/) WU T D.
PA   (ZHOU/) ZHOU Y.
XX
PI   Wu TD,  Zhou Y;
XX
DR   WPI; 2004-534300/51.
XX
PT   New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT   preventing or treating cell proliferative disorders such as cancer.
XX
PS   Claim 1; SEQ ID NO 1793; 5504pp; English.
XX
CC   The present invention describes an isolated tumour-associated antigenic
CC   target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC   sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC   (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC   sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC   (c). Also described: (1) an expression vector comprising the above
CC   nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC   a process for producing a polypeptide; (4) an isolated polypeptide
CC   comprising: (a) an amino acid sequence encoded by any of the above
```

CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 2767 BP; 621 A; 809 C; 853 G; 484 T; 0 U; 0 Other;

Query Match 99.5%; Score 214; DB 12; Length 2767;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 362 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 421

Qy 61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 422 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 481

Qy 121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 482 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 541

Qy 181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
||||||||||||||||||||||||||||||||||
Db 542 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 575

RESULT 9
ADQ83802
ID ADQ83802 standard; cDNA; 2767 BP.
XX
AC ADQ83802;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #616.
XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004060270-A2.
XX
PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
XX
PR 18-OCT-2002; 2002US-0418988P.
XX
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
PI Wu TD, Zhou Y;
XX
DR WPI; 2004-534300/51.
XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
PS Claim 1; SEQ ID NO 616; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 2767 BP; 621 A; 808 C; 854 G; 484 T; 0 U; 0 Other;

Query Match 99.5%; Score 214; DB 13; Length 2767;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 362 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 421

Qy 61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 422 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 481

Qy 121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 482 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 541

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Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||||||||||||||||||||||||||||
Db        542 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 575
```

RESULT 10
ADS89095
ID ADS89095 standard; DNA; 5387 BP.
XX
AC ADS89095;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human HSPA1A gene SEQ ID NO:111.
XX
KW ds; gene; human; cell proliferative disorder; breast; methylation;
KW cytostatic; gene therapy; single nucleotide polymorphism; SNP.
XX
OS Homo sapiens.
XX
PN WO2004035803-A2.
XX
PD 29-APR-2004.
XX
PF 01-OCT-2003; 2003WO-EP010881.
XX
PR 01-OCT-2002; 2002DE-01045779.
PR 07-JAN-2003; 2003DE-01000096.
PR 17-APR-2003; 2003DE-01017955.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
XX
DR WPI; 2004-348468/32.
XX
PT Predicting responsiveness of a subject with breast cell proliferative
PT disorder, useful for treating or differentiating breast cell
PT proliferative disorders comprises analyzing methylation pattern of a
PT genomic DNA from the subject.
XX
PS Example 2; SEQ ID NO 111; 104pp; English.
XX
CC The invention relates to a novel method for predicting the responsiveness
CC of a subject with a cell proliferative disorder of the breast tissues to
CC a therapy comprising analysing the methylation pattern of a target
CC nucleic acid by contacting at least one of the target nucleic acids in a
CC biological sample obtained from the subject prior to or during treatment.
CC The method of the invention has cytostatic activity, and may have a use
CC in gene therapy. The set of oligonucleotides comprising at least two of
CC the oligomers are useful for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC methods, nucleic acid, oligonucleotide, and kit are useful for the
CC treatment, characterisation, classification and/or differentiation, of
CC breast cell proliferative disorders. The method is also useful for
CC predicting the responsiveness of a subject with a cell proliferative
CC disorder of the breast tissues to a therapy. The present sequence is used
CC in the exemplification of the invention.
XX
SQ Sequence 5387 BP; 1291 A; 1506 C; 1471 G; 1119 T; 0 U; 0 Other;

```
  Query Match             99.5%;  Score 214;  DB 13;  Length 5387;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-54;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1982 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 2041

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2042 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 2101

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2102 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 2161

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||||||||||||||||||||||||||||
Db       2162 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 2195
```

RESULT 11
ADA45212
ID ADA45212 standard; DNA; 549 BP.
XX
AC ADA45212;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human hsp70 gene 5' promoter region.
XX
KW gene; ds; human; tumour mass; cancer; bone marrow;
KW endothelial cell precursor; ECP; cytostatic;
KW tumour angiogenesis inhibitor; gene therapy; cell therapy; angiogenesis;
KW hsp70; promoter.
XX
OS Homo sapiens.
XX
PN WO2003061591-A2.
XX
PD 31-JUL-2003.
XX
PF 22-JAN-2003; 2003WO-US001827.
XX
PR 22-JAN-2002; 2002US-0349345P.
XX
PA (ADCE-) ADVANCED CELL TECHNOLOGY INC.
XX
PI West MD;
XX
DR WPI; 2003-598707/56.
XX
PT Decreasing tumor mass in a patient comprises grafting genetically
PT modified endothelial cell precursors into the patient.
XX
PS Example 3; Fig 1; 34pp; English.
XX
CC The invention relates to a novel method for decreasing tumour mass in a
CC cancer patient. The method comprises ablating bone marrow from the
CC patient and grafting endothelial cell precursors (ECPs), or their
CC precursors, into the patient such that a decrease in tumour mass results,
CC where the ECPs or their precursors are genetically modified to mediate a
CC decrease in tumour mass. The method of the invention has cytostatic
CC activity. A polynucleotide of the invention acts as a tumour angiogenesis
CC inhibitor, and may have a use in gene therapy and cell therapy.
CC Genetically modified endothelial cell precursors are useful for
CC decreasing tumour mass in a cancer patient. This is particularly useful
CC for inhibiting and/or disrupting angiogenesis of the tumours, and
CC consequently inhibiting tumour growth and killing tumour cells. The
CC present sequence represents the 5' promoter region of the human hsp70
CC gene.
XX
SQ Sequence 549 BP; 110 A; 174 C; 167 G; 98 T; 0 U; 0 Other;

```
  Query Match             99.3%;  Score 213.4;  DB 9;  Length 549;
  Best Local Similarity   99.5%;  Pred. No. 2.4e-54;
  Matches  214;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 328

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        329 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 388

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 448

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              ||||||||| ||||||||||||||||||||||||||
Db        449 TCTCAGAGCGGAGCCGACAGAGAGCAGGGAACCGC 483


RESULT 12
AAT58086
ID   AAT58086 standard; cDNA; 2465 BP.
XX
AC   AAT58086;
XX
DT   24-OCT-1997  (first entry)
XX
DE   Human heat shock protein 70 cDNA.
XX
KW   Human; heat shock protein 70; HSP70; primer; probe; detection;
KW   intracellular; abnormal transcription; acute; chronic; sustained; stress;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             263. .2185
FT                   /*tag= a
FT                   /product= "HSP70"
XX
PN   JP08322577-A.
XX
PD   10-DEC-1996.
XX
PF   01-JUN-1995;   95JP-00158581.
XX
PR   01-JUN-1995;   95JP-00158581.
XX
PA   (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
DR   WPI; 1997-081088/08.
DR   P-PSDB; AAW10065.
XX
PT   Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific
PT   primer or probe, used in detection of human acute and chronic sustained
PT   stress load.
XX
PS   Claim 1; Fig 1; 13pp; Japanese.
XX
CC   The present sequence, which encodes human heat shock protein 70 (HSP70),
CC   is located on human chromosome 6p 21.3-22 and 14q 22-24 and 21. Primers
CC   and probes based on the HSP70 cDNA coding sequence can be used to detect
CC   the abnormal transcription of intracellular HSP70 mRNA in human acute and
CC   chronic sustained stress load
XX
SQ   Sequence 2465 BP; 553 A; 713 C; 758 G; 441 T; 0 U; 0 Other;

  Query Match            99.3%;  Score 213.4;  DB 2;  Length 2465;
  Best Local Similarity   99.5%;  Pred. No. 3.4e-54;
  Matches  214;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         48 ATAACGGCTAGCCTGAGGAGCTGCTGCCACAGTCCACTACCTTTTTCGAGAGTGACTCCC 107

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 167

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        168 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 227

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              ||||||||||||||||||||||||||||||||||||
Db        228 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 262


RESULT 13
ADO01084
ID   ADO01084 standard; DNA; 213 BP.
XX
AC   ADO01084;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human hsp70 translational enhancer element DNA sequence SEQ ID NO:6.
XX
KW   increasing glycogen; toxic; toxic glycogen level; glycogen;
KW   cell proliferative disorder; tumour therapy; tumour; anti-tumour therapy;
KW   anti-cell proliferative; cytostatic; gene therapy; sarcoma; melanoma;
KW   myeloma; blastoma; glioma; lymphoma; leukaemia; human;
KW   heat shock protein 70; chromosome 6; hsp70; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004039412-A2.
XX
PD   13-MAY-2004.
XX
PF   29-OCT-2003; 2003WO-IB005562.
XX
PR   29-OCT-2002; 2002US-0422365P.
XX
PA   (ENGE-) ENGENE INC.
XX
PI   Doiron B,  Pownall S,  Cheung A,  Hsu E;
XX
DR   WPI; 2004-376072/35.
DR   GENBANK; M11717.
XX
PT   Increasing glycogen to toxic levels in a cell, useful for treating cell
PT   proliferative disorder, comprises expressing in a cell a gene product
PT   that increases the amount of glycogen to toxic levels in the cell.
XX
PS   Example 1; SEQ ID NO 6; 98pp; English.
XX
CC   The present invention describes a method for increasing glycogen to toxic
CC   levels in a cell. The method comprises expressing in a cell a gene
CC   product that increases the amount of glycogen to toxic levels in the
CC   cell. Also described: (1) treating a cell proliferative disorder in a
CC   subject, where the cell proliferative disorder is not a liver, muscle or
CC   brain cell disorder, by expressing in one or more cells comprising the
CC   disorder a gene product that increases the amount of intracellular
CC   glycogen, or contacting one or more cells comprising the disorder with an
CC   agent that increases the amount of intracellular glycogen, sufficient to
CC   treat the cell proliferative disorder; (2) treating a subject that is
CC   undergoing or has undergone tumour therapy, where the tumour therapy was
CC   not for liver, muscle or brain tumour by administering to the subject an
CC   agent in an amount that increases the amount of intracellular glycogen in
CC   a cell; (3) increasing effectiveness of an anti-tumour therapy; (4)
CC   identifying an agent (A) having anti-cell proliferative activity; and (5)
CC   a kit comprising the agent, and instructions for administering the agent
CC   to a subject in need or treatment on a label or packaging insert. (A) has
CC   cytostatic activity, and can be used in gene therapy. The methods are
CC   useful for treating a cell proliferative disorder, e.g. tumour, such as
CC   sarcoma, melanoma, myeloma, blastoma, glioma, lymphoma or leukaemia. The
CC   present sequence represents a translation enhancer element in the 5'
CC   untranslated region of a human heat shock protein 70 (hsp70) sequence
CC   comprising nucleotides 276 to 488 from the human hsp70 nucleotide
CC   sequence of GenBank accession number M11717, which is used in an example
CC   from the present invention. Human hsp70 is located on chromosome 6, more
CC   specifically 6p21.3.
XX
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SQ   Sequence 213 BP; 40 A; 71 C; 63 G; 39 T; 0 U; 0 Other;

  Query Match            99.1%;  Score 213;  DB 12;  Length 213;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-54;
  Matches  213;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGT 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGT 60

Qy         63 TGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCC 120

Qy        123 GGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATC 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATC 180

Qy        183 TCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              |||||||||||||||||||||||||||||||||
Db        181 TCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 213


RESULT 14
AAA97541
ID   AAA97541 standard; cDNA; 2700 BP.
XX
AC   AAA97541;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human Hsp72 (heat shock protein 72) cDNA.
XX
KW   Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;
KW   expression modulator; JNK phosphatase inhibitor; antiproliferative;
KW   drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma;
KW   carcinoma; breast cancer; prostate cancer; premalignant condition; ss.
XX
OS   Homo sapiens.
XX
PN   WO200054814-A1.
XX
PD   21-SEP-2000.
XX
PF   17-MAR-2000; 2000WO-US007350.
XX
PR   18-MAR-1999;   99US-0125046P.
XX
PA   (PHYL-) PHYLOGENY INC.
XX
PI   Volloch VZ,  Sherman M;
XX
DR   WPI; 2000-647056/62.
DR   P-PSDB; AAB23252.
XX
PT   Identifying compounds that inhibit proliferation of cells and capable of
PT   modulating the expression of heat shock protein 72 gene and/or activity
PT   of Hsp72 useful for treating cancers such as leukemia, lymphoma.
XX
PS   Example; Fig 16A; 77pp; English.
XX
CC   The invention relates to a novel method of identifying compounds that
CC   inhibit proliferation of cells comprising contacting a test compound with
CC   a cell which overexpresses Hsp72 (heat shock protein 72), and determining
CC   if the test compound inhibits activity or expression of Hsp72.
CC   Optionally, Hsp72 is contacted with the test compound under optimum
CC   conditions to allow the two components to interact and bind, forming a
CC   complex which is detected. The invention also relates to a method of
CC   identifying compounds that inhibit Hsp72-mediated JNK phosphatase
CC   activation, comprising contacting a test compound with a cell which
CC   expresses Hsp72, exposing the cell to a heat induced stress and
CC   determining if the compound inhibits JNK phosphatase activity. The
CC   invention additionally encompasses compositions comprising an inhibitor
CC   of Hsp72 or JNK phosphatase activity. The compounds identified as
CC   inhibitors of Hsp72 or JNK phosphatase activity are useful for inhibiting
CC   the proliferation of cells. Modulation of the activity of the JNK
CC   phosphatase or Hsp72 is used to treat a proliferative disorder such as
CC   cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and
CC   carcinomas, breast cancer, prostate cancer). The compounds that inhibit
CC   Hsp72 activity can also be administered to treat premalignant conditions
CC   and to prevent progression to a neoplastic or malignant state. The
CC   compounds that inhibit Hsp72 function are administered to a patient
CC   having a disease or disorder mediated by an increase of Hsp72 expression
CC   or activity relative to normal levels. The present sequence represents
CC   cDNA encoding human Hsp72 used in the exemplifications of the invention
XX
SQ   Sequence 2700 BP; 601 A; 780 C; 834 G; 485 T; 0 U; 0 Other;

  Query Match            98.8%;  Score 212.4;  DB 3;  Length 2700;
  Best Local Similarity  99.5%;  Pred. No. 6.9e-54;
  Matches  213;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
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Db        274 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 393

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 453

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||| ||||||||||||||||||||||||
Db        454 TCTCAGAGCGGAGCCGACAGAGAGCAGGGAACCG 487


RESULT 15
ADM02338
ID   ADM02338 standard; cDNA; 1903 BP.
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AC   ADM02338;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human cDNA of the invention SEQ ID NO:1023.
XX
KW   ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS   Homo sapiens.
XX
PN   EP1347046-A1.
XX
PD   24-SEP-2003.
XX
PF   12-APR-2002; 2002EP-00008400.
XX
PR   22-MAR-2002; 2002JP-00137785.
XX
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Sugiyama T,  Otsuki T,  Wakamatsu A,  Sato H,  Ishii S;
PI   Yamamoto J,  Isono Y,  Hio Y,  Otsuka K,  Nagai K,  Irie R,  Tamechika I;
PI   Seki N,  Yoshikawa T,  Otsuka M,  Nagahari K,  Masuho Y;
XX
DR   WPI; 2003-723558/69.
DR   P-PSDB; ADM04781.
XX
PT   New polynucleotides and polypeptides are useful in gene therapy, for
PT   developing a diagnostic marker or medicines for regulating their
PT   expression and activity, or as a target of gene therapy.
XX
PS   Claim 1; SEQ ID NO 1023; 305pp; English.
XX
```

CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC cDNA sequence of the invention.
XX
SQ Sequence 1903 BP; 425 A; 531 C; 590 G; 357 T; 0 U; 0 Other;

Query Match 97.9%; Score 210.4; DB 11; Length 1903;
Best Local Similarity 99.5%; Pred. No. 2.6e-53;
Matches 211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          3 AACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGT 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGT 60

Qy         63 TGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCC 120

Qy        123 GGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATC 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATC 180

Qy        183 TCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||| ||||||||||||||||||||||||
Db        181 TCAGAGCGGAGCCGACAGAGAGCAGGGAACCG 212
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Search completed: February 11, 2005, 08:17:28
Job time : 224 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2005, 07:52:23 ; Search time 87 Seconds
(without alignments)
4043.672 Million cell updates/sec

Title: US-09-936-506-1
Perfect score: 215
Sequence: 1 ataacggctagcctgaggag.....gacagagagcagggaaccgc 215

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	215	100.0	533	1	US-07-975-719-2	Sequence 2, Appli
	2	215	100.0	533	1	US-08-599-825-2	Sequence 2, Appli
	3	215	100.0	533	2	US-09-048-488-2	Sequence 2, Appli
	4	215	100.0	2691	3	US-08-955-565A-1	Sequence 1, Appli
	5	191.4	89.0	2412	4	US-09-919-039-144	Sequence 144, App
	6	187.4	87.2	420	4	US-09-621-976-827	Sequence 827, App
	7	156.8	72.9	2458	4	US-09-919-039-145	Sequence 145, App
	8	99.2	46.1	1941	4	US-09-976-594-996	Sequence 996, App
	9	36.6	17.0	750	1	US-07-975-719-1	Sequence 1, Appli
	10	36.6	17.0	750	1	US-08-599-825-1	Sequence 1, Appli
	11	36.6	17.0	750	2	US-09-048-488-1	Sequence 1, Appli
c	12	33.6	15.6	1074	4	US-09-252-991A-11809	Sequence 11809, A
c	13	33.6	15.6	1320	4	US-09-252-991A-11869	Sequence 11869, A
	14	32.4	15.1	205	4	US-09-313-294A-6467	Sequence 6467, Ap
c	15	32.4	15.1	1728	4	US-09-902-540-4475	Sequence 4475, Ap
	16	32.4	15.1	28172	4	US-09-902-540-1221	Sequence 1221, Ap
	17	32.2	15.0	17938	4	US-09-902-540-1111	Sequence 1111, Ap
c	18	31.8	14.8	4722	3	US-08-979-608A-14	Sequence 14, Appl
c	19	31.8	14.8	4722	4	US-09-517-849-14	Sequence 14, Appl
c	20	31.8	14.8	4722	4	US-09-616-289-14	Sequence 14, Appl
c	21	31.8	14.8	27825	4	US-09-949-016-17483	Sequence 17483, A
	22	31.6	14.7	1196	1	US-08-167-939A-5	Sequence 5, Appli
	23	31.6	14.7	1196	1	US-08-567-538-5	Sequence 5, Appli
	24	31.4	14.6	601	4	US-09-949-016-17939	Sequence 17939, A
	25	31.4	14.6	601	4	US-09-949-016-125345	Sequence 125345,
	26	31.4	14.6	601	4	US-09-949-016-125356	Sequence 125356,
	27	31.4	14.6	11752	4	US-09-949-016-11756	Sequence 11756, A
	28	31.4	14.6	11865	4	US-09-949-016-15297	Sequence 15297, A
	29	31.4	14.6	11865	4	US-09-949-016-15298	Sequence 15298, A
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	31	30.8	14.3	15132	4	US-09-902-540-1137	Sequence 1137, Ap
c	32	30.4	14.1	603	4	US-09-902-540-9070	Sequence 9070, Ap
c	33	30.4	14.1	834	4	US-09-621-976-2574	Sequence 2574, Ap
c	34	30.4	14.1	7719	4	US-09-902-540-969	Sequence 969, App
c	35	30	14.0	10419	4	US-09-408-020-3	Sequence 3, Appli
c	36	30	14.0	19157	4	US-09-949-016-13142	Sequence 13142, A
c	37	30	14.0	42432	4	US-09-408-020-2	Sequence 2, Appli
	38	29.6	13.8	601	4	US-09-949-016-30895	Sequence 30895, A
	39	29.6	13.8	601	4	US-09-949-016-30896	Sequence 30896, A
	40	29.6	13.8	601	4	US-09-949-016-105265	Sequence 105265,
	41	29.6	13.8	601	4	US-09-949-016-105266	Sequence 105266,
	42	29.6	13.8	16572	4	US-09-949-016-12409	Sequence 12409, A
	43	29.6	13.8	16578	4	US-09-949-016-14680	Sequence 14680, A
	44	29.6	13.8	107800	4	US-09-949-016-13118	Sequence 13118, A
	45	29.6	13.8	116425	4	US-09-949-016-11809	Sequence 11809, A

ALIGNMENTS

RESULT 1
US-07-975-719-2
; Sequence 2, Application US/07975719
; Patent No. 5521084
; GENERAL INFORMATION:
; APPLICANT: KOWALSKI, JACEK
; APPLICANT: GILBERT, SCOTT
; APPLICANT: ZAMB, TIMOTHY J.
; TITLE OF INVENTION: BOVINE HEAT SHOCK PROMOTER AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBERTA L. ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/975,719
; FILING DATE: 19921113
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 533 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-975-719-2

Query Match 100.0%; Score 215; DB 1; Length 533;
Best Local Similarity 100.0%; Pred. No. 5.6e-57;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
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Db        235 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 294
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Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
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Db        295 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 354

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
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Db        355 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 414

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
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Db        415 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 449


RESULT 2
US-08-599-825-2
; Sequence 2, Application US/08599825
; Patent No. 5733745
;  GENERAL INFORMATION:
;    APPLICANT:  KOWALSKI, JACEK
;    APPLICANT:  GILBERT, SCOTT
;    APPLICANT:  ZAMB, TIMOTHY J.
;    TITLE OF INVENTION:  BOVINE HEAT SHOCK PROMOTER AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROBERTA L. ROBINS
;      STREET:  285 HAMILTON AVENUE, SUITE 200
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/599,825
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ROBINS, ROBERTA L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  9001-0003.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 327-3400
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  533 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-599-825-2

  Query Match             100.0%;  Score 215;  DB 1;  Length 533;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-57;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        235 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 294

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 354

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 414

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
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Db        415 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 449


RESULT 3
US-09-048-488-2
; Sequence 2, Application US/09048488
; Patent No. 5981224
;  GENERAL INFORMATION:
;    APPLICANT:  KOWALSKI, JACEK
;    APPLICANT:  GILBERT, SCOTT
;    APPLICANT:  ZAMB, TIMOTHY J.
;    TITLE OF INVENTION:  BOVINE HEAT SHOCK PROMOTER AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROBERTA L. ROBINS
;      STREET:  635 BRYANT STREET
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/048,488
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/975,719
;      FILING DATE:  1992-11-13
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ROBINS, ROBERTA L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  9001-0003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  533 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-048-488-2

  Query Match             100.0%;  Score 215;  DB 2;  Length 533;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-57;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
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Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
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Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              |||||||||||||||||||||||||||||||||||
Db        415 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 449


RESULT 4
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```
US-08-955-565A-1
; Sequence 1, Application US/08955565A
; Patent No. 6331388
; GENERAL INFORMATION:
;  APPLICANT: Malkovsky, Miroslav
;  APPLICANT:  Wells, Andrew
;  TITLE OF INVENTION: Immune Response Enhancer Therapy
;  FILE REFERENCE: WARF-02625
;  CURRENT APPLICATION NUMBER: US/08/955,565A
;  CURRENT FILING DATE:  1997-10-17
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 2691
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-955-565A-1

  Query Match             100.0%;  Score 215;  DB 3;  Length 2691;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-57;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        274 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 393

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 453

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
              ||||||||||||||||||||||||||||||||||
Db        454 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 488


RESULT 5
US-09-919-039-144
; Sequence 144, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 401
;  SOFTWARE: PERL Program
; SEQ ID NO 144
;   LENGTH: 2412
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6727066 242010.16
US-09-919-039-144

  Query Match             89.0%;  Score 191.4;  DB 4;  Length 2412;
  Best Local Similarity   99.0%;  Pred. No. 1.7e-49;
  Matches  203;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         11 GCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAA 70
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAA 60

Qy         71 GGCTTCCCAGAGCGAACCTGT-GCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCC 129
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         61 GGCTTCCCAGAGCGAACCTGTGGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCC 120

Qy        130 GGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGC 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGC 180

Qy        190 CGAGCCGACAGAGAGCAGGGAACCG 214
              |||||||||||||||||||||||||
Db        181 GGAGCCGACAGAGAGCAGGGAACCG 205


RESULT 6
US-09-621-976-827
; Sequence 827, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 827
;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 218..418
US-09-621-976-827

  Query Match             87.2%;  Score 187.4;  DB 4;  Length 420;
  Best Local Similarity   97.7%;  Pred. No. 1.8e-48;
  Matches  210;  Conservative    1;  Mismatches    2;  Indels    2;  Gaps    2;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 61

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 121

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTT-CCGTTTCCAGCCCCCA 179
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        122 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTYCCGTTTCCAGCCCCCA 181

Qy        180 ATCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              |||||||||| || :||||| ||||||||||||||
Db        182 ATCTCAGAGCGGA-SCGACATAGAGCAGGGAACCG 215


RESULT 7
US-09-919-039-145
; Sequence 145, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 401
;  SOFTWARE: PERL Program
; SEQ ID NO 145
;   LENGTH: 2458
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
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;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6727066 1678695CB1
US-09-919-039-145

  Query Match             72.9%;  Score 156.8;  DB 4;  Length 2458;
  Best Local Similarity   88.5%;  Pred. No. 8.6e-39;
  Matches  170;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy         11 GCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAA 70
              ||||||||||||||||||  |||| || | | |||||||||||||||||  |||||||
Db          1 GCCTGAGGAGCTGCTGCGAGGGTCCGCTTCGTCTTTCGAGAGTGACTCCCGCGGTCCCAA 60

Qy         71 GGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCG 130
              ||||| ||||||||||||||||||||||||||||||| || ||||||||||||| |
Db         61 GGCTTTCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGTGTTGAGTTTCCGGCGTTCC 120

Qy        131 GAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCC 190
              ||||||| |||||||| |||||||||| ||   |||||||||||||||| |||||||||
Db        121 GAAGGACTGAGCTCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCCAGTCTCAGAGCG 180

Qy        191 GAGCCGACAGAG 202
              ||||| ||||||
Db        181 GAGCCCACAGAG 192


RESULT 8
US-09-976-594-996
; Sequence 996, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 996
;   LENGTH: 1941
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 242010.60
US-09-976-594-996

  Query Match             46.1%;  Score 99.2;  DB 4;  Length 1941;
  Best Local Similarity   89.2%;  Pred. No. 5.3e-21;
  Matches  107;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy         83 CGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAGC 142
              |||||||||||||||||||||||||||| || |||||||||||| | ||||||| ||||
Db          1 CGAACCTGTGCGGCTGCAGGCACCGGCGTGTTGAGTTTCCGGCGTTCCGAAGGACTGAGC 60

Qy        143 TCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACAGAG 202
              |||| |||||||||| ||   |||||||||||||||| ||||||||| ||||| ||||||
Db         61 TCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCCAGTCTCAGAGCGGAGCCCACAGAG 120


RESULT 9
US-07-975-719-1
; Sequence 1, Application US/07975719
; Patent No. 5521084
;  GENERAL INFORMATION:
;    APPLICANT:  KOWALSKI, JACEK
;    APPLICANT:  GILBERT, SCOTT
;    APPLICANT:  ZAMB, TIMOTHY J.
;    TITLE OF INVENTION:  BOVINE HEAT SHOCK PROMOTER AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROBERTA L. ROBINS
;      STREET:  635 BRYANT STREET
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/975,719
;      FILING DATE:  19921113
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ROBINS, ROBERTA L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  9001-0003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  750 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-975-719-1

  Query Match             17.0%;  Score 36.6;  DB 1;  Length 750;
  Best Local Similarity   66.0%;  Pred. No. 0.096;
  Matches   68;  Conservative    0;  Mismatches   34;  Indels    1;  Gaps    1;

Qy        101 GGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAGC-TCTTCTCGCGGATCCAG 159
              |||||| | ||||  ||||| |||  |||| || | |||||| |||  |||| |||||
Db        552 GGCACCAGAGCGTTCAGTTTTCGGGTTCCGAAAAGCCCGAGCTTCTCGTCGCAGATCCTC 611

Qy        160 TGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACAGAG 202
              |   ||| || |||     || || |   | ||||||  | ||
Db        612 TTCACCGATTTCAGGTTTGAAGCTTATTTCGGAGCCGGAAAAG 654


RESULT 10
US-08-599-825-1
; Sequence 1, Application US/08599825
; Patent No. 5733745
;  GENERAL INFORMATION:
;    APPLICANT:  KOWALSKI, JACEK
;    APPLICANT:  GILBERT, SCOTT
;    APPLICANT:  ZAMB, TIMOTHY J.
;    TITLE OF INVENTION:  BOVINE HEAT SHOCK PROMOTER AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROBERTA L. ROBINS
;      STREET:  285 HAMILTON AVENUE, SUITE 200
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/599,825
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
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```
;      NAME:  ROBINS, ROBERTA L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  9001-0003.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 327-3400
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  750 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-599-825-1

  Query Match             17.0%;  Score 36.6;  DB 1;  Length 750;
  Best Local Similarity   66.0%;  Pred. No. 0.096;
  Matches   68;  Conservative    0;  Mismatches   34;  Indels    1;  Gaps    1;

Qy        101 GGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAGC-TCTTCTCGCGGATCCAG 159
              |||||| | ||||  ||||| |||  |||| || | |||||| |||  |||| |||||
Db        552 GGCACCAGAGCGTTCAGTTTTCGGGTTCCGAAAAGCCCGAGCTTCTCGTCGCAGATCCTC 611

Qy        160 TGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACAGAG 202
              |   ||| || |||     || || |   | ||||||  | ||
Db        612 TTCACCGATTTCAGGTTTGAAGCTTATTTCGGAGCCGGAAAAG 654


RESULT 11
US-09-048-488-1
; Sequence 1, Application US/09048488
; Patent No. 5981224
;  GENERAL INFORMATION:
;    APPLICANT:  KOWALSKI, JACEK
;    APPLICANT:  GILBERT, SCOTT
;    APPLICANT:  ZAMB, TIMOTHY J.
;    TITLE OF INVENTION:  BOVINE HEAT SHOCK PROMOTER AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROBERTA L. ROBINS
;      STREET:  635 BRYANT STREET
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/048,488
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/975,719
;      FILING DATE:  1992-11-13
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ROBINS, ROBERTA L.
;      REGISTRATION NUMBER:  33,208
;      REFERENCE/DOCKET NUMBER:  9001-0003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 617-8999
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  750 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-048-488-1

  Query Match             17.0%;  Score 36.6;  DB 2;  Length 750;
  Best Local Similarity   66.0%;  Pred. No. 0.096;
  Matches   68;  Conservative    0;  Mismatches   34;  Indels    1;  Gaps    1;

Qy        101 GGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAGC-TCTTCTCGCGGATCCAG 159
              |||||| | ||||  ||||| |||  |||| || | |||||| |||  |||| |||||
Db        552 GGCACCAGAGCGTTCAGTTTTCGGGTTCCGAAAAGCCCGAGCTTCTCGTCGCAGATCCTC 611

Qy        160 TGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACAGAG 202
              |   ||| || |||     || || |   | ||||||  | ||
Db        612 TTCACCGATTTCAGGTTTGAAGCTTATTTCGGAGCCGGAAAAG 654


RESULT 12
US-09-252-991A-11809/c
; Sequence 11809, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 11809
;   LENGTH: 1074
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11809

  Query Match             15.6%;  Score 33.6;  DB 4;  Length 1074;
  Best Local Similarity   59.4%;  Pred. No. 0.9;
  Matches   57;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy         82 GCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAG 141
              |||| |||||||||| |||||   |    |||||||||| ||||| | | |  |   | |
Db        828 GCGATCCTGTGCGGTTGCAGCGCCATCGGCGTCGAGTTGCCGGCCTGCAGGCGCTTCAGG 769

Qy        142 CTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCC 177
                 ||   | |    ||  ||||    |||| |||
Db        768 GAGATCGGCCAGTCGTAGGCTTCCCAGCCCAGGCCC 733


RESULT 13
US-09-252-991A-11869/c
; Sequence 11869, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 11869
;   LENGTH: 1320
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11869

  Query Match             15.6%;  Score 33.6;  DB 4;  Length 1320;
  Best Local Similarity   59.4%;  Pred. No. 0.95;
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  Matches   57;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy          82 GCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAG 141
               |||| ||||||||| |||||    |    |||||||||| ||||| | | |   |   | |
Db        1103 GCGATCCTGTGCGGTTGCAGCGCCATCGGCGTCGAGTTGCCGGCCTGCAGGCGCTTCAGG 1044

Qy         142 CTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCC 177
                 ||   | |    ||  ||||    |||| |||
Db        1043 GAGATCGGCCAGTCGTAGGCTTCCCAGCCCAGGCCC 1008


RESULT 14
US-09-313-294A-6467
; Sequence 6467, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
;  APPLICANT:  Lalgudi, Raghunath V.
;  APPLICANT:  Ito, Laura Y.
;  APPLICANT:  Sherman, Bradley K.
;  TITLE OF INVENTION:  POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
;  FILE REFERENCE:  PL-0017 US
;  CURRENT APPLICATION NUMBER: US/09/313,294A
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS:  7600
;  SOFTWARE:  PERL Program
; SEQ ID NO 6467
;   LENGTH: 205
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6476212 700351854H1
;   NAME/KEY: unsure
;   LOCATION: 31, 178, 202-203
;   OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6467

  Query Match             15.1%;  Score 32.4;  DB 4;  Length 205;
  Best Local Similarity   68.2%;  Pred. No. 1.3;
  Matches   45;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         149 CGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACAGAGAGCAGG 208
               | |||| | || | | ||||| | |||   | |  | ||||||||||||| ||||  || |
Db          80 CACGGAGCAAGAGATTCGTTTGCTGCCATTATTAACCGAGCCGAGCCGAGAGAGGTCAAG 139

Qy         209 GAACCG 214
                 ||| |
Db         140 CAACGG 145


RESULT 15
US-09-902-540-4475/c
; Sequence 4475, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4475
;   LENGTH: 1728
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-4475

  Query Match             15.1%;  Score 32.4;  DB 4;  Length 1728;
  Best Local Similarity   50.0%;  Pred. No. 2.4;
  Matches   81;  Conservative    0;  Mismatches   81;  Indels    0;  Gaps    0;

Qy          16 AGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAAGGCTT 75
               |||| |||||||| ||  |      | | |||||   ||| ||||||   |     |||
Db        1628 AGGAACTGCTGCGCCACGCGGTCCACCTCTTCGACCTTGAGTCCCGTGAGCAGCGCGCTC 1569

Qy          76 CCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGG 135
               || |       | || || | ||      |   | | | |||     |  |  ||  |||
Db        1568 GCCTGCCGCGCGCGGTCCGCCAGCGCCGTCTCACCCATGGAGCCGTGGATGCGCGTCAGG 1509

Qy         136 ACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCC 177
               ||  |    | ||  ||     |  | ||||   ||||| ||
Db        1508 GCCAGGTGGATTTCCGGGTCGAACGGGTCCGACGCCAGCGCC 1467


Search completed: February 11, 2005, 09:04:16
Job time : 89 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2005, 08:35:16 ; Search time 259 Seconds
(without alignments)
4898.065 Million cell updates/sec

Title: US-09-936-506-1
Perfect score: 215
Sequence: 1 ataacggctagcctgaggag.....gacagagagcagggaaccgc 215

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	214	99.5	2732	18	US-10-335-053-291	Sequence 291, App
2	213.4	99.3	549	17	US-10-348-359-1	Sequence 1, Appli
3	210.4	97.9	1903	17	US-10-108-260A-1023	Sequence 1023, Ap
4	195	90.7	2387	17	US-10-172-118-1144	Sequence 1144, Ap
5	195	90.7	2387	17	US-10-342-887-1144	Sequence 1144, Ap
6	191.4	89.0	2412	10	US-09-919-039-144	Sequence 144, App
c 7	163.6	76.1	506	16	US-10-029-386-6557	Sequence 6557, Ap
8	158.2	73.6	284	18	US-10-425-115-89981	Sequence 89981, A
9	156.8	72.9	2458	10	US-09-919-039-145	Sequence 145, App
10	156.8	72.9	2513	18	US-10-335-053-290	Sequence 290, App
c 11	156.4	72.7	2771	13	US-10-027-632-111980	Sequence 111980,
c 12	156.4	72.7	2771	17	US-10-027-632-111980	Sequence 111980,
c 13	145.2	67.5	595	18	US-10-363-345A-17429	Sequence 17429, A
14	145.2	67.5	595	18	US-10-363-345A-17430	Sequence 17430, A
c 15	145.2	67.5	596	18	US-10-363-345A-20731	Sequence 20731, A
16	145.2	67.5	596	18	US-10-363-345A-20732	Sequence 20732, A
c 17	145.2	67.5	9899	15	US-10-311-455-2415	Sequence 2415, Ap
c 18	145.2	67.5	3673778	16	US-10-312-841-2	Sequence 2, Appli
19	134	62.3	595	18	US-10-363-345A-17431	Sequence 17431, A
c 20	134	62.3	595	18	US-10-363-345A-17432	Sequence 17432, A
21	134	62.3	596	18	US-10-363-345A-20729	Sequence 20729, A
c 22	134	62.3	596	18	US-10-363-345A-20730	Sequence 20730, A
23	134	62.3	9899	15	US-10-311-455-2416	Sequence 2416, Ap
24	134	62.3	3673778	16	US-10-312-841-1	Sequence 1, Appli
25	116.6	54.2	2460	18	US-10-370-715B-21	Sequence 21, Appl
c 26	103.4	48.1	583	18	US-10-363-345A-17425	Sequence 17425, A
27	103.4	48.1	583	18	US-10-363-345A-17426	Sequence 17426, A
28	99.6	46.3	583	18	US-10-363-345A-17427	Sequence 17427, A
c 29	99.6	46.3	583	18	US-10-363-345A-17428	Sequence 17428, A
c 30	89.2	41.5	584	18	US-10-363-345A-20735	Sequence 20735, A
31	89.2	41.5	584	18	US-10-363-345A-20736	Sequence 20736, A
32	83.8	39.0	584	18	US-10-363-345A-20733	Sequence 20733, A
c 33	83.8	39.0	584	18	US-10-363-345A-20734	Sequence 20734, A
c 34	58	27.0	939	16	US-10-029-386-20724	Sequence 20724, A
35	38.4	17.9	2636	13	US-10-002-600-95	Sequence 95, Appl
36	34.2	15.9	2940917	13	US-10-027-632-174763	Sequence 174763,
37	34.2	15.9	2940917	17	US-10-027-632-174763	Sequence 174763,
38	32.8	15.3	1473	17	US-10-282-122A-14406	Sequence 14406, A
39	32.4	15.1	2261	17	US-10-389-566-273	Sequence 273, App
40	32.2	15.0	7789	17	US-10-333-314-38	Sequence 38, Appl
41	32.2	15.0	9698	17	US-10-210-130-37	Sequence 37, Appl
42	32.2	15.0	9807	17	US-10-379-381-1	Sequence 1, Appli
43	32.2	15.0	9930	17	US-10-210-130-33	Sequence 33, Appl
44	32.2	15.0	10122	17	US-10-210-130-35	Sequence 35, Appl
45	32.2	15.0	62805	17	US-10-379-381-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-335-053-291
; Sequence 291, Application US/10335053
; Publication No. US20040241653A1
; GENERAL INFORMATION:
; APPLICANT: Quark Biotech, Inc.
; TITLE OF INVENTION: Methods for identifying marker genes for cancer
; FILE REFERENCE: 68733-A; 070/US1
; CURRENT APPLICATION NUMBER: US/10/335,053
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 60/345,317
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 291
; LENGTH: 2732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-335-053-291

Query Match 99.5%; Score 214; DB 18; Length 2732;
Best Local Similarity 100.0%; Pred. No. 2.4e-60;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
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Db        274 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 393

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        394 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 453

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
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Db        454 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 487
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RESULT 2
US-10-348-359-1
; Sequence 1, Application US/10348359
; Publication No. US20040018178A1
; GENERAL INFORMATION:
; APPLICANT: WEST, MICHAEL
; TITLE OF INVENTION: STEM CELL-DERIVED ENDOTHELIAL CELLS MODIFIED TO DISRUPT
; TITLE OF INVENTION: TUMOR ANGIOGENESIS
; FILE REFERENCE: 100375.54374US
; CURRENT APPLICATION NUMBER: US/10/348,359
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/349,345
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-348-359-1

Query Match 99.3%; Score 213.4; DB 17; Length 549;
Best Local Similarity 99.5%; Pred. No. 3.4e-60;
Matches 214; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 328

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 388

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 448

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
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Db        449 TCTCAGAGCGGAGCCGACAGAGAGCAGGGAACCGC 483
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RESULT 3
US-10-108-260A-1023
; Sequence 1023, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1023
; LENGTH: 1903
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-1023

Query Match 97.9%; Score 210.4; DB 17; Length 1903;
Best Local Similarity 99.5%; Pred. No. 3.6e-59;
Matches 211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          3 AACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGT 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGT 60

Qy         63 TGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCC 120

Qy        123 GGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATC 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATC 180

Qy        183 TCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||| ||||||||||||||||||||||||
Db        181 TCAGAGCGGAGCCGACAGAGAGCAGGGAACCG 212
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RESULT 4
US-10-172-118-1144
; Sequence 1144, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1144
; LENGTH: 2387
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_005345
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1144

Query Match 90.7%; Score 195; DB 17; Length 2387;
Best Local Similarity 100.0%; Pred. No. 4.2e-54;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         20 GCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAAGGCTTCCCA 79
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Db          1 GCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAAGGCTTCCCA 60

Qy         80 GAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCG 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCG 120

Qy        140 AGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACA 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACA 180

Qy        200 GAGAGCAGGGAACCG 214
              |||||||||||||||
Db        181 GAGAGCAGGGAACCG 195
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RESULT 5
US-10-342-887-1144
; Sequence 1144, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.

```
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Christopher J.
;  APPLICANT:  Van 't Veer, Laura Johanna
;  APPLICANT:  Van de Vijver, Marc J.
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-188-999
;  CURRENT APPLICATION NUMBER: US/10/342,887
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: 60/298,918
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: 60/380,710
;  PRIOR FILING DATE: 2002-05-14
;  PRIOR APPLICATION NUMBER: 10/172,118
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1144
;   LENGTH: 2387
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-342-887-1144

  Query Match             90.7%;  Score 195;  DB 17;  Length 2387;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-54;
  Matches  195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 GCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAAGGCTTCCCA 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAAGGCTTCCCA 60

Qy         80 GAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCG 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCG 120

Qy        140 AGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACA 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACA 180

Qy        200 GAGAGCAGGGAACCG 214
              |||||||||||||||
Db        181 GAGAGCAGGGAACCG 195


RESULT 6
US-09-919-039-144
; Sequence 144, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 401
;  SOFTWARE: PERL Program
; SEQ ID NO 144
;   LENGTH: 2412
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030108871A1 242010.16
US-09-919-039-144

  Query Match             89.0%;  Score 191.4;  DB 10;  Length 2412;
  Best Local Similarity   99.0%;  Pred. No. 6.4e-53;
  Matches  203;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         11 GCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAA 70
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Db          1 GCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAA 60

Qy         71 GGCTTCCCAGAGCGAACCTGT-GCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCC 129
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         61 GGCTTCCCAGAGCGAACCTGTGGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCC 120

Qy        130 GGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGC 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGC 180

Qy        190 CGAGCCGACAGAGAGCAGGGAACCG 214
              |||||||||||||||||||||||||
Db        181 GGAGCCGACAGAGAGCAGGGAACCG 205


RESULT 7
US-10-029-386-6557/c
; Sequence 6557, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 6557
;   LENGTH: 506
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AF134726.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.5
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.8
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL =  11
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.9
;   OTHER INFORMATION: SWISSPROT HIT: P08107, EVALUE 2.00e-17
;   OTHER INFORMATION: NT HIT: M59830.1, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: BG773197.1, EVALUE 0.00e+00
US-10-029-386-6557

  Query Match             76.1%;  Score 163.6;  DB 16;  Length 506;
  Best Local Similarity   88.1%;  Pred. No. 7.9e-44;
  Matches  178;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              | |||||| ||||||||||||||||||||  |||| || | | ||||||||||||||||||
Db        339 AAAACGGCCAGCCTGAGGAGCTGCTGCGAGGGTCCGCTTCGTCTTTCGAGAGTGACTCCC 280

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              |  |||||||||||| ||||||||||||||||||||||||||||||||| || ||||||
Db        279 GCGGTCCCAAGGCTTTCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGTGTTGAGTTT 220

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||| | ||||||| |||||||| |||||||||| ||   ||||||||||||||||
Db        219 CCGGCGTTCCGAAGGACTGAGCTCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCCAG 160

Qy        181 TCTCAGAGCCGAGCCGACAGAG 202
              ||||||||| ||||| ||||||
Db        159 TCTCAGAGCGGAGCCCACAGAG 138


RESULT 8
US-10-425-115-89981
; Sequence 89981, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
```

```
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 89981
;   LENGTH: 284
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_182065C.1
US-10-425-115-89981

  Query Match             73.6%;  Score 158.2;  DB 18;  Length 284;
  Best Local Similarity   95.3%;  Pred. No. 4.5e-42;
  Matches  163;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         45 TTCGAGAGTGACTCCCGTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCA 104
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db          1 TTCGAGAGTGACTCCCGTTGTCACAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCA 60

Qy        105 CCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTC 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGGCGCGTCGAGTTTCCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTC 120

Qy        165 CGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
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Db        121 CGTTTCCAGCCCCCAATCTCATAGCGGAGCCGACAGATAGCAGGATCCGGC 171


RESULT 9
US-09-919-039-145
; Sequence 145, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
;  APPLICANT: Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
;  FILE REFERENCE: PA-0035 US
;  CURRENT APPLICATION NUMBER: US/09/919,039
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 60/222,113
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 401
;  SOFTWARE: PERL Program
; SEQ ID NO 145
;   LENGTH: 2458
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030108871A1 1678695CB1
US-09-919-039-145

  Query Match             72.9%;  Score 156.8;  DB 10;  Length 2458;
  Best Local Similarity   88.5%;  Pred. No. 1.5e-41;
  Matches  170;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy         11 GCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAA 70
              |||||||||||||||||  |||| || | | ||||||||||||||||||  |||||||
Db          1 GCCTGAGGAGCTGCTGCGAGGGTCCGCTTCGTCTTTCGAGAGTGACTCCCGCGGTCCCAA 60

Qy         71 GGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCG 130
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCTTTCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGTGTTGAGTTTCCGGCGTTCC 120

Qy        131 GAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCC 190
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGGACTGAGCTCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCCAGTCTCAGAGCG 180

Qy        191 GAGCCGACAGAG 202
              |||||||||||||
Db        181 GAGCCCACAGAG 192


RESULT 10
US-10-335-053-290
; Sequence 290, Application US/10335053
; Publication No. US20040241653A1
; GENERAL INFORMATION:
;  APPLICANT: Quark Biotech, Inc.
;  TITLE OF INVENTION: Methods for identifying marker genes for cancer
;  FILE REFERENCE: 68733-A; 070/US1
;  CURRENT APPLICATION NUMBER: US/10/335,053
;  CURRENT FILING DATE:  2003-03-27
;  PRIOR APPLICATION NUMBER: 60/345,317
;  PRIOR FILING DATE: 2001-12-31
;  NUMBER OF SEQ ID NOS: 319
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 290
;   LENGTH: 2513
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-335-053-290

  Query Match             72.9%;  Score 156.8;  DB 18;  Length 2513;
  Best Local Similarity   88.5%;  Pred. No. 1.5e-41;
  Matches  170;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy         11 GCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAA 70
              |||||||||||||||||  |||| || | | ||||||||||||||||||  |||||||
Db          1 GCCTGAGGAGCTGCTGCGAGGGTCCGCTTCGTCTTTCGAGAGTGACTCCCGCGGTCCCAA 60

Qy         71 GGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCG 130
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCTTTCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGTGTTGAGTTTCCGGCGTTCC 120

Qy        131 GAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCC 190
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGGACTGAGCTCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCCAGTCTCAGAGCG 180

Qy        191 GAGCCGACAGAG 202
              |||||||||||||
Db        181 GAGCCCACAGAG 192


RESULT 11
US-10-027-632-111980/c
; Sequence 111980, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111980
```

```
;   LENGTH: 2771
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-111980

  Query Match             72.7%;  Score 156.4;  DB 13;  Length 2771;
  Best Local Similarity   99.4%;  Pred. No. 2.1e-41;
  Matches  157;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 101

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 41

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCA 158
              |||||||||||||||||||||||||||||| ||||
Db         40 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGCTCCA 3


RESULT 12
US-10-027-632-111980/c
; Sequence 111980, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111980
;   LENGTH: 2771
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-111980

  Query Match             72.7%;  Score 156.4;  DB 17;  Length 2771;
  Best Local Similarity   99.4%;  Pred. No. 2.1e-41;
  Matches  157;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 101

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 41

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCA 158
              |||||||||||||||||||||||||||||| ||||
Db         40 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGCTCCA 3


RESULT 13
US-10-363-345A-17429/c
; Sequence 17429, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: E01/1227
;  CURRENT APPLICATION NUMBER: US/10/363,345A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 17429
;   LENGTH: 595
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 17429
US-10-363-345A-17429

  Query Match             67.5%;  Score 145.2;  DB 18;  Length 595;
  Best Local Similarity   79.9%;  Pred. No. 8.9e-38;
  Matches  171;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              |||||| ||| ||| |  | || || ||||| ||||||||||||||||| | | ||||||
Db        454 ATAACGACTAACCTAAAAAACTACTACGACAATCCACTACCTTTTTCGAAAATAACTCCC 395

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||| ||||||  ||||||| | ||||||| | || || ||  ||||| |||||||| |||
Db        394 GTTATCCCAAAACTTCCCAAAACGAACCTATACGACTACAAACACCGACGCGTCGAATTT 335

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||| |||||| ||  ||||| |||||||||| ||||| | |||||||||| |||||||
Db        334 CCGACGTCCGAAAAAACCGAACTCTTCTCGCGAATCCAATATTCCGTTTCCAACCCCCAA 275

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||| | |||| |||||| | | ||   |||||
Db        274 TCTCAAAACCGAACCGACAAAAAACAAAAAACCG 241


RESULT 14
US-10-363-345A-17430
; Sequence 17430, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: E01/1227
;  CURRENT APPLICATION NUMBER: US/10/363,345A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 17430
;   LENGTH: 595
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 17430
US-10-363-345A-17430

  Query Match             67.5%;  Score 145.2;  DB 18;  Length 595;
  Best Local Similarity   79.9%;  Pred. No. 8.9e-38;
  Matches  171;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              |||||| ||| ||| |  | || || ||||| ||||||||||||||||| | | ||||||
Db        142 ATAACGACTAACCTAAAAAACTACTACGACAATCCACTACCTTTTTCGAAAATAACTCCC 201
```

```
Qy          61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
               ||| ||||||  ||||||| | ||||||| | || || ||  ||||| |||||||| |||
Db         202 GTTATCCCAAAACTTCCCAAAACGAACCTATACGACTACAAACACCGACGCGTCGAATTT 261

Qy         121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
               ||| |||||| ||  ||||| |||||||||||| ||||| | |||||||||||| |||||||
Db         262 CCGACGTCCGAAAAAACCGAACTCTTCTCGCGAATCCAATATTCCGTTTCCAACCCCCAA 321

Qy         181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
               ||||| | |||| |||||| | | ||   |||||
Db         322 TCTCAAAACCGAACCGACAAAAAACAAAAAACCG 355


RESULT 15
US-10-363-345A-20731/c
; Sequence 20731, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
;  APPLICANT: Alexander Olek
;  APPLICANT:  Christian Piepenbrock
;  APPLICANT:  Kurt Berlin
;  TITLE OF INVENTION: Method for determining the degree of methylation of defined
;  TITLE OF INVENTION:  cytosines in genomic DNA in the sequence context of 5'-CpG-3
;  FILE REFERENCE: E01/1227
;  CURRENT APPLICATION NUMBER: US/10/363,345A
;  CURRENT FILING DATE:  2003-03-03
;  NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 20731
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   OTHER INFORMATION: CpG-island No: 20731
US-10-363-345A-20731

  Query Match             67.5%;  Score 145.2;  DB 18;  Length 596;
  Best Local Similarity   79.9%;  Pred. No. 8.9e-38;
  Matches  171;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy           1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
               |||||| ||| ||| |  | || || ||||| |||||||||||||||| | | ||||||
Db         545 ATAACGACTAACCTAAAAAACTACTACGACAATCCACTACCTTTTTCGAAAATAACTCCC 486

Qy          61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
               ||| ||||||  ||||||| | ||||||| | || || ||  ||||| |||||||| |||
Db         485 GTTATCCCAAAACTTCCCAAAACGAACCTATACGACTACAAACACCGACGCGTCGAATTT 426

Qy         121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
               ||| |||||| ||  ||||| |||||||||||| ||||| | |||||||||||| |||||||
Db         425 CCGACGTCCGAAAAAACCGAACTCTTCTCGCGAATCCAATATTCCGTTTCCAACCCCCAA 366

Qy         181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
               ||||| | |||| |||||| | | ||   |||||
Db         365 TCTCAAAACCGAACCGACAAAAAACAAAAAACCG 332


Search completed: February 11, 2005, 09:47:21
Job time : 265 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 11, 2005, 07:40:18 ; Search time 1641 Seconds
(without alignments)
4987.092 Million cell updates/sec

Title: US-09-936-506-1
Perfect score: 215
Sequence: 1 ataacggctagcctgaggag.....gacagagagcagggaaccgc 215

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	214	99.5	642	7	CN397686	CN397686 170005326
2	214	99.5	2380	3	CR605652	CR605652 full-leng
3	214	99.5	2383	3	CR598680	CR598680 full-leng
4	214	99.5	2387	3	CR626292	CR626292 full-leng
5	214	99.5	2391	3	CR608110	CR608110 full-leng
6	214	99.5	2396	3	CR599258	CR599258 full-leng
7	214	99.5	2398	3	CR618761	CR618761 full-leng
8	214	99.5	2398	3	CR621778	CR621778 full-leng
9	214	99.5	2399	3	CR606872	CR606872 full-leng
10	214	99.5	2401	3	CR595673	CR595673 full-leng
11	214	99.5	2409	3	CR624878	CR624878 full-leng
12	214	99.5	2417	3	CR603812	CR603812 full-leng
13	212.4	98.8	356	6	CB112917	CB112917 K-EST0154
14	212.4	98.8	493	5	BQ639435	BQ639435 he15e11.y
15	212.4	98.8	511	6	CB154948	CB154948 K-EST0213
16	212.4	98.8	527	6	CB141518	CB141518 K-EST0195
17	212.4	98.8	590	6	CB138426	CB138426 K-EST0191
18	212.4	98.8	701	4	BG773197	BG773197 602721934
19	212.4	98.8	816	4	BG485554	BG485554 602505445
20	212.4	98.8	916	4	BI462679	BI462679 603202121
21	212	98.6	582	5	BP350439	BP350439 BP350439
22	211.4	98.3	751	4	BI464037	BI464037 603202811
23	211	98.1	570	5	BP259174	BP259174 BP259174
24	210.8	98.0	582	5	BP245573	BP245573 BP245573
25	210.8	98.0	584	5	BP232134	BP232134 BP232134
26	210.4	97.9	267	1	AU076824	AU076824 AU076824
27	210.4	97.9	316	4	BM822968	BM822968 K-EST0093
28	210.4	97.9	376	6	CB133590	CB133590 K-EST0184
29	210.4	97.9	409	6	CB133685	CB133685 K-EST0184
30	210.4	97.9	436	4	BI548281	BI548281 603191148
31	210.4	97.9	463	6	CB137170	CB137170 K-EST0189
32	210.4	97.9	479	6	CB133251	CB133251 K-EST0184
33	210.4	97.9	505	6	CB133452	CB133452 K-EST0184
34	210.4	97.9	509	6	CB134000	CB134000 K-EST0185
35	210.4	97.9	509	6	CB138961	CB138961 K-EST0191
36	210.4	97.9	516	6	CB137829	CB137829 K-EST0190
37	210.4	97.9	516	6	CB138598	CB138598 K-EST0191
38	210.4	97.9	522	6	CB133993	CB133993 K-EST0185
39	210.4	97.9	523	6	CB152005	CB152005 K-EST0209
40	210.4	97.9	523	6	CB152693	CB152693 K-EST0209
41	210.4	97.9	526	5	BP382960	BP382960 BP382960
42	210.4	97.9	532	6	CB153107	CB153107 K-EST0210
43	210.4	97.9	533	6	CB133518	CB133518 K-EST0184
44	210.4	97.9	546	6	CB155190	CB155190 K-EST0213
45	210.4	97.9	581	5	BP231177	BP231177 BP231177

ALIGNMENTS

RESULT 1
CN397686
LOCUS CN397686 642 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000532601385 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN397686
VERSION CN397686.1 GI:47385281
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 642)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 642 Std Error: 0.00.
FEATURES Location/Qualifiers
source 1. .642
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
/clone_lib="GRN_ES"
/note="oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"
ORIGIN

Query Match 99.5%; Score 214; DB 7; Length 642;
Best Local Similarity 100.0%; Pred. No. 6.6e-51;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 137
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```
Qy          61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         138 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 197

Qy         121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         198 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 257

Qy         181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
               ||||||||||||||||||||||||||||||||||
Db         258 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 291


RESULT 2
CR605652
LOCUS       CR605652                2380 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DF033YK03 of Fetal brain of Homo sapiens
            (human).
ACCESSION   CR605652
VERSION     CR605652.1  GI:50486459
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2380)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2380)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .2380
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF033YK03"
                     /tissue_type="Fetal brain"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match            99.5%;  Score 214;  DB 3;  Length 2380;
  Best Local Similarity  100.0%;  Pred. No. 7.9e-51;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          14 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 73

Qy          61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          74 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 133

Qy         121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         134 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 193

Qy         181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
               ||||||||||||||||||||||||||||||||||
Db         194 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 227


RESULT 3
CR598680
LOCUS       CR598680                2383 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DC028YM15 of Neuroblastoma Cot
            25-normalized of Homo sapiens (human).
ACCESSION   CR598680
VERSION     CR598680.1  GI:50479487
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2383)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2383)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .2383
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DC028YM15"
                     /tissue_type="Neuroblastoma Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match            99.5%;  Score 214;  DB 3;  Length 2383;
  Best Local Similarity  100.0%;  Pred. No. 7.9e-51;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          14 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 73

Qy          61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          74 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 133

Qy         121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         134 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 193

Qy         181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
               ||||||||||||||||||||||||||||||||||
Db         194 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 227


RESULT 4
CR626292
LOCUS       CR626292                2387 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DF038YK05 of Fetal brain of Homo sapiens
            (human).
ACCESSION   CR626292
VERSION     CR626292.1  GI:50507099
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2387)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2387)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .2387
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF038YK05"
                     /tissue_type="Fetal brain"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             99.5%;  Score 214;  DB 3;  Length 2387;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-51;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 73

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 133

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 193

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              |||||||||||||||||||||||||||||||||
Db        194 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 227


RESULT 5
CR608110
LOCUS       CR608110                2391 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DJ004YG01 of T cells (Jurkat cell line)
            Cot 10-normalized of Homo sapiens (human).
ACCESSION   CR608110
VERSION     CR608110.1  GI:50488917
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2391)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2391)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .2391
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DJ004YG01"
                     /tissue_type="T cells (Jurkat cell line) Cot
                     10-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             99.5%;  Score 214;  DB 3;  Length 2391;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-51;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 88

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 148

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 208

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              |||||||||||||||||||||||||||||||||
Db        209 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 242


RESULT 6
CR599258
LOCUS       CR599258                2396 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DF007YE19 of Fetal brain of Homo sapiens
            (human).
ACCESSION   CR599258
VERSION     CR599258.1  GI:50480065
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2396)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2396)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .2396
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /db_xref="taxon:9606"
                     /clone="CS0DF007YE19"
                     /tissue_type="Fetal brain"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             99.5%;  Score 214;  DB 3;  Length 2396;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-51;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 73

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 133

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 193

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||||||||||||||||||||||||||||
Db        194 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 227


RESULT 7
CR618761
LOCUS       CR618761               2398 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DN003YF07 of Adult brain of Homo sapiens
            (human).
ACCESSION   CR618761
VERSION     CR618761.1  GI:50499568
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2398)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2398)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .2398
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DN003YF07"
                     /tissue_type="Adult brain"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             99.5%;  Score 214;  DB 3;  Length 2398;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-51;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 88

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 148

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 208

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||||||||||||||||||||||||||||
Db        209 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 242


RESULT 8
CR621778
LOCUS       CR621778               2398 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DE003YF16 of Placenta of Homo sapiens
            (human).
ACCESSION   CR621778
VERSION     CR621778.1  GI:50502585
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2398)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2398)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .2398
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE003YF16"
                     /tissue_type="Placenta"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             99.5%;  Score 214;  DB 3;  Length 2398;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-51;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 73

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 133

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 193

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
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Db        194 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 227


RESULT 9
CR606872
LOCUS       CR606872               2399 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DF021YI09 of Fetal brain of Homo sapiens
            (human).
ACCESSION   CR606872
VERSION     CR606872.1  GI:50487679
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2399)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2399)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .2399
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF021YI09"
                     /tissue_type="Fetal brain"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             99.5%;  Score 214;  DB 3;  Length 2399;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-51;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 73

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 133

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 193

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||||||||||||||||||||||||||||
Db        194 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 227


RESULT 10
CR595673
LOCUS       CR595673               2401 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DE002YK13 of Placenta of Homo sapiens
            (human).
ACCESSION   CR595673
VERSION     CR595673.1  GI:50476480
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2401)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2401)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .2401
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE002YK13"
                     /tissue_type="Placenta"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             99.5%;  Score 214;  DB 3;  Length 2401;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-51;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 88

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 148

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 208

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||||||||||||||||||||||||||||
Db        209 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 242


RESULT 11
CR624878
LOCUS       CR624878               2409 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DF012YA23 of Fetal brain of Homo sapiens
            (human).
ACCESSION   CR624878
VERSION     CR624878.1  GI:50505685
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2409)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2409)
  AUTHORS   Genoscope.
```

```
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .2409
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF012YA23"
                     /tissue_type="Fetal brain"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             99.5%;  Score 214;  DB 3;  Length 2409;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-51;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 73

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 133

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 193

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||||||||||||||||||||||||||||
Db        194 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 227


RESULT 12
CR603812
LOCUS       CR603812                2417 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DF020YJ02 of Fetal brain of Homo sapiens
            (human).
ACCESSION   CR603812
VERSION     CR603812.1  GI:50484619
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2417)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 2417)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .2417
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF020YJ02"
                     /tissue_type="Fetal brain"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             99.5%;  Score 214;  DB 3;  Length 2417;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-51;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 88

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 148

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 208

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||||||||||||||||||||||||||||
Db        209 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 242


RESULT 13
CB112917
LOCUS       CB112917                356 bp    mRNA    linear   EST 28-JAN-2003
DEFINITION  K-EST0154803 L6ChoCK0 Homo sapiens cDNA clone L6ChoCK0-10-A11 5',
            mRNA sequence.
ACCESSION   CB112917
VERSION     CB112917.1  GI:27938724
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 356)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 10  row: A  column: 11
            High quality sequence stop: 356.
FEATURES             Location/Qualifiers
     source          1. .356
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="L6ChoCK0-10-A11"
                     /sex="M"
                     /cell_line="Cho-CK"
                     /lab_host="Top10F'"
                     /clone_lib="L6ChoCK0"
                     /note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including
                     EcoRI site by treatment of T4 RNA ligase and the first
                     strand cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
```

adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 98.8%; Score 212.4; DB 6; Length 356;
Best Local Similarity 99.5%; Pred. No. 1.7e-50;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||| |||||||||||||||||||||||||
Db        181 TCTCAGAGCGGAGCCGACAGAGAGCAGGGAACCG 214
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RESULT 14
BQ639435
LOCUS BQ639435 493 bp mRNA linear EST 15-JUL-2002
DEFINITION he15e11.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he Homo sapiens cDNA clone he15e11 5', mRNA sequence.
ACCESSION BQ639435
VERSION BQ639435.1 GI:21763894
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 493)
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
TITLE Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts
JOURNAL Mol. Vis. 8 (4), 196-204 (2002)
MEDLINE 22103461
PUBMED 12107411
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 15 row: e column: 11
Seq primer: M13RP1 reverse primer (ABI).
FEATURES Location/Qualifiers
source 1. .493
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="he15e11"
/tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Retina cDNA (Un-normalized, unamplified): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 98.8%; Score 212.4; DB 5; Length 493;
Best Local Similarity 99.5%; Pred. No. 1.8e-50;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60
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Db         10 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 69

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 129

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 189

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
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Db        190 TCTCAGAGCGGAGCCGACAGAGAGCAGGGAACCG 223
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RESULT 15
CB154948
LOCUS CB154948 511 bp mRNA linear EST 29-JAN-2003
DEFINITION K-EST0213039 B2N807043 Homo sapiens cDNA clone B2N807043-30-G11 5', mRNA sequence.
ACCESSION CB154948
VERSION CB154948.1 GI:28140051
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 511)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 30 row: G column: 11
High quality sequence stop: 511.
FEATURES Location/Qualifiers
source 1. .511
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="B2N807043-30-G11"
/sex="M"
/lab_host="Top10F'"
/clone_lib="B2N807043"
/note="Organ: Brain; Vector: pCNS-D2; Site_1: EcoRI;

Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 98.8%; Score 212.4; DB 6; Length 511;
Best Local Similarity 99.5%; Pred. No. 1.8e-50;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db          1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 60

Qy         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120

Qy        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180

Qy        181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
              ||||||||| ||||||||||||||||||||||||
Db        181 TCTCAGAGCGGAGCCGACAGAGAGCAGGGAACCG 214
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Search completed: February 11, 2005, 09:02:43
Job time : 1646 secs